a) contacting the repertoire with the generic ligand to select polypeptides bound thereto, thereby obtaining a first selected pool of binding polypeptides; and

b) contacting the first selected pool of polypeptides with a target ligand to select a population of polypeptides which bind to the target ligand.

34. (New) The method of claim 33 wherein said repertoire of polypeptides is first contacted with said target ligand, and the resulting selected pool of binding polypeptides is then contacted with said generic ligand.

35. (New) The method of claim 33 wherein said generic ligand binds a subset of the members of said repertoire of polypeptides.

36. (New) The method of claim 33 wherein the binding polypeptide is a member of the immunoglobulin superfamily.

37. (New) The method of claim 38 wherein the binding polypeptide is an antibody or T-cell receptor polypeptide.

38. (New) The method of claim 36 wherein the binding polypeptide comprises V_H, V_β, V_L or V_α polypeptide sequence.

39. (New) The method of claim 36 wherein the binding polypeptide is an scFv polypeptide.

40. (New) The method of claim 33 wherein said repertoire is comprised by phage particles.

41. (New) The method of claim 40 wherein said phage particles comprise a fusion polypeptide.

42. (New) The method of claim 33 wherein said generic ligand is a superantigen.

43. (New) The method of claim 42 wherein said superantigen is selected from Protein A, Protein L and Protein G.

44. (New) The method of claim 33 wherein polypeptides in said repertoire are varied at random positions.

45. (New) The method of claim 44 wherein the variation is achieved by individually incorporating all 20 different amino acids at positions to be varied.

46. (New) The method of claim 44 wherein the variation is achieved by individually incorporating fewer than all different amino acids at positions to be varied.

47. (New) The method of claim 33 wherein polypeptides in said repertoire are varied at selected positions.

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48. (New) The method of claim 47 wherein said selected positions are comprised by the binding site for the target ligand.

49. (New) The method of claim 47 wherein said selected positions are a subset of those within the binding site for the target ligand.

50. (New) The method of claim 47 wherein the variation is achieved by individually incorporating all 20 different amino acids at positions to be varied.

51. (New) The method of claim 47 wherein the variation is achieved by individually incorporating fewer than all different amino acids at positions to be varied.

52. (New) The method of claim 33 wherein step (a) further comprises the steps of:

i) contacting a second repertoire of polypeptides with a second generic ligand to select polypeptides bound thereto, thereby obtaining a second selected pool of binding polypeptides, and

ii) combining said first and said second selected pools of binding polypeptides to create a third repertoire;

wherein step (b) comprises contacting said third repertoire with said target ligand to select a population of polypeptides which bind to said target ligand.

REMARKS

Elections under the Restriction Requirement: